



1/31

17

	1				50
EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAS.
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLSATVQAN
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA</u>	<u>SATV-TAVLA</u>	<u>TLL-ATVQA-</u>

C1

	51				100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.VTED	SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRVA	VLIVNSDKEG	TGEKEKVEEN	SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG	TGEKEKVEEN	SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG	NGENE.STGN	IGWSIYYDNH
P20	ATDTD...EDE	ELESVARSAL	VLQFMIDKEG	NGEIESTGDI	GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG	SGELET...I	SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG	SVELET...I	SLSMTNDSKE
Consensus	-----	-L--V-R--	V-----EG	--E-E-----	-----

V1

	101				150
EG327	GVLTAGTITL	KAGDNLKIKQ	NTNENTNASSFTYSLK	KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSSFTYSLK	KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK	KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK	KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNTNENT	NDSSFTYSLK	KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD.....FTYSLK	KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK	KDLTGGLINVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK	KDLTGGLINVE
Consensus	----- <u>TL</u>	<u>KAGDNLKIKQ</u>	-----	---- <u>FTYSLK</u>	<u>K-L--L--V-</u>

V1

C2

V2

C3

FIG. 1A



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	151				200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE	TNGDTTVHLN	GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H41	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDML
Consensus	TEKLSF-AN-	-KVNI-SDTK	GLNFAK-TA-	TNGD-TVHLN	GIGSTLTD-L

C3

	201				250
EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVPK	GSTTGQSENV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVPK	GSTTGQSENV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVPK	GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN	AGWNIKGVPK	G-T-----NV

V3

C4

V4

	251				300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVESKDNGK	-TEVKIGAKT	SVIKEKDGL

C5

FIG. 1B



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	301				350
EG327	VTGKDKGEND	SSTDKGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
BZ198	VTGKGKDENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
BZ10	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H15	VTGKGKDENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
EG329	VTGKDKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
PMC21	VTGKDKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H38	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
P20	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
Z2491	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
H41	VTGKGKGENG	SSTDEGEGLV	TAKEVIDAVN	KAGWRMKTTT	ANGQTGQADK
Consensus	<u>VTGK-K-EN-</u>	<u>SSTD-GEGLV</u>	<u>TAKEVIDAVN</u>	<u>KAGWRMKTTT</u>	<u>ANGQTGQADK</u>

C5

	351				400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN	TVMYDVNVGD	ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGN	TVKYDVNVGD	ALNVNQLQNS
Consensus	<u>FETVTSGT-V</u>	<u>TFASG-GTTA</u>	<u>TVSKDDQGN</u>	<u>TV-YDVNVGD</u>	<u>ALNVNQLQNS</u>

C5

	401				450
EG327	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
BZ198	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
BZ10	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
H15	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
EG329	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
PMC21	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
H38	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
P20	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
Z2491	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EISRNGKNID
H41	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
Consensus	<u>GWNLDSKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE</u>	<u>TVNINAGNNI</u>	<u>EI-RNGKNID</u>

C5

FIG. 1C



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	451		500
EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDTNK PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA LNVGSKDANK PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A LNVGSK--NK PVRITNVAPG</u>

C5

	501		550
EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA RAGIAQAIAT AGL-QAYLPG</u>

C5

	551		600
EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW IIKGTASGNS RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW -IKGTASGNS RGHFG-SASV</u>

C5

FIG. 1D



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	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

FIG. 1E

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C1

C1

C1

V1

FIG. 2A

[illegible]

V1

	281							350
H15	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA	
BZ10	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA	
BZ198	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA	
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA	
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA	
Z2491	AACGACAGCA	AGGAATTTGT	AGACCCATAC	ATAGTA...	.GTTACCCTC	AAAGCCGGCG	ACAACCTGAA	
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	CATACATAGT	AGTTACCCTC	AAAGCCGGCG	ACAACCTGAA	
EG329	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA	
PMC21	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA	
EG327	GAGTATATTT	CGACAAGAAA	GGAGTACTAA	CAGCCGGAAC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA	
Consensus	-----A---	-----	-----	-----	--T-ACCCTC	AAAGCCGGCG	ACAACCTGAA	

V1

C2

	351							420
H15	AATCAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA	
BZ10	AATCAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA	
BZ198	AATCAACAA	AACACCAATG	AAAACACC..	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA	
P20	AATCAACAA	AGCGGCAAAG	A.....CTTCACCTA	CTCGCTGAAA	
H38	AATCAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA	
Z2491	AATCAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA	
H41	AATCAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA	
EG329	AATCAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA	
PMC21	AATCAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA	
EG327	AATCAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA	
Consensus	<u>AATCAACAA</u>	<u>A-C-----</u>	<u>-----</u>	<u>-----</u>	<u>-----</u>	<u>-CTTCACCTA</u>	<u>CTC-CTGAAA</u>	

C2

V2

C3

FIG. 2B



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	421		490
H15	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
BZ10	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
BZ198	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
P20	AAAGAGCTGA	AAGACCTGAC	CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
H38	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AATAAAGTCA
Z2491	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AAGAAAGTCA
H41	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AAGAAAGTCA
EG329	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA ACTGAAAAAT TATCGTTTAG CGCAAACGGC AATAAAGTCA
PMC21	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA ACTGAAAAAT TATCGTTTAG CGCAAACGGC AATAAAGTCA
EG327	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA ACTGAAAAAT TATCGTTTAG CGCAAACAGC AATAAAGTCA
Consensus	AAAGA-CT-A	-AG--CTGA-	CA-TGTTG-A ACTGAAAAAT TATCGTTT-G CGCAAAC-G- AA-AAAGTCA

C3

	491		560
H15	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
BZ10	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
BZ198	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
P20	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
H38	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TC GCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
Z2491	ACATCATAAG	CGACACCAAA	GGCTTGAATT TC GCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
H41	ACATCATAAG	CGACACCAAA	GGCTTGAATT TC GCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
EG329	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
PMC21	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
EG327	ACATCACAAAG	CGACACCAAA	GGCTTGAATT TC GCGAAAAA AACGGCTGAG ACCAACGGCG ACACCACGGT
Consensus	ACATCA-AAG	CGACACCAAA	GGCTTGAATT T-GCGAAA-A AACGGCTG-G AC-AACGGCG AC-CCACGGT

C3

	561		630
H15	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
BZ10	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
BZ198	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
P20	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
H38	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
Z2491	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
H41	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATATGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
EG329	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
PMC21	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
EG327	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
Consensus	TCATCTGAAC	GGTAT-GGTT	CGACTTTGAC CGATA-GCT- --G--T-C-- --GC--C-- ----G--C-

C3

V3

FIG.2C



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	631						700
H15	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ10	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ198	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
P20	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCGGCAA	GTATTAAAGA	TGTGTTGAAT	GCAGGCTGGA
H38	AACGACAACG	TTACCGATGA	CAAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Z2491	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCGGCAA	GTATTAAAGA	TGTGTTGAAT	GCAGGCTGGA
H41	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG329	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
PMC21	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG327	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Consensus	----AC-A--	-TAC--AT-A	C-----A--	CGTGC-GCAA	G--TTAA-GA	-GT-TT-AA-	GC-GG-TGGA
	V3			C4			
	701						770
H15	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
BZ10	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTC	GATTTCGTCC	GCACTTACGA
BZ198	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
P20	ATATTAAAGG	TGTTAAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H38	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
Z2491	ATATTAAAGG	TGTTAAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H41	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG329	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
PMC21	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG327	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
Consensus	A-ATTAA-GG	-GTTAA-C-	GG--CAACA-	CT-----TC	-GA-AA-GT-	GATTTCGTCC	-CACTTACGA
	C4		V4		C5		
	771						840
H15	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ10	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ198	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
P20	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H38	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Z2491	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H41	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG329	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
PMC21	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG327	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Consensus	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
	C5						
	841						910
H15	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ10	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ198	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
P20	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H38	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Z2491	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H41	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG329	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
PMC21	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG327	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Consensus	A-AACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTAT-A	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
	C5						

FIG. 2D



10/31

911 980
H15 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
B210 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
BZ198 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
P20 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
H38 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
Z2491 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
H41 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
EG329 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
PMC21 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
EG327 AAGACAAAGG CGAGAATGAT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
Consensus AAG-CAAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA

C5

981 1050
H15 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
B210 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
BZ198 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
P20 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
H38 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
Z2491 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
H41 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
EG329 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
PMC21 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
EG327 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
Consensus TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG

C5

1051 1120
H15 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
B210 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
BZ198 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
P20 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
H38 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
Z2491 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
H41 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
EG329 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
PMC21 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
EG327 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAAATGG TACAACGCG ACTGTAAGTA
Consensus TTTGAAACCG TTACATCAGG CACAAA-GTA ACCTTTGCTA GTGGTAA-GG TACAACGCG ACTGTAAGTA

C5

1121 1190
H15 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
B210 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
BZ198 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
P20 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
H38 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
Z2491 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
H41 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
EG329 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
PMC21 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
EG327 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
Consensus AAGATGATCA AGGCAACATC ACTGTTA-GT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT

C5

FIG. 2E



11/31

1191 1260
H15 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
B210 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
B2198 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
P20 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
H38 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
Z2491 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
H41 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
EG329 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
PMC21 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
EG327 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
Consensus GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT

C5

1261 1330
H15 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
B210 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
B2198 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
P20 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H38 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Z2491 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H41 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG329 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
PMC21 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG327 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Consensus GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC

C5

1331 1400
H15 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
B210 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
B2198 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
P20 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H38 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Z2491 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H41 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG329 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
PMC21 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG327 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Consensus GCAACGG-AA AAATATCGAC ATCGCCACTT CGATG-C-CC GCA-TTTTCC AGCGTTTCGC TCGG-CGCGGG

C5

1401 1470
H15 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
B210 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
B2198 GGCGGATGCG CCCACTTTGA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TACCAACAAA
P20 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
H38 GGCGGATGCG CCCACTTTGA GCGTGGATGA CAAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Z2491 GGCAGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
H41 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
EG329 GGCGGATGCG CCCACTTTGA GCGTGGAT.. .GGGGACGCA TTGAATGTCG GCAGCAAGGA GGACAACAAA
PMC21 GGCGGATGCG CCCACTTTGA GCGTGGAT.. .GGGGACGCA TTGAATGTCG GCAGCAAGGA GGACAACAAA
EG327 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Consensus GGC-GATGCG CCCACTTT-A GCGTGGAT-- --GG-CGC- TTGAATGTCG GCAGCAAG-A ---CAACAAA

C5

FIG. 2F



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1471 1540
H15 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
BZ10 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
BZ198 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
P20 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
H38 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
Z2491 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
H41 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCG CAACTTAAAG
EG329 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
PMC21 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
EG327 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
Consensus CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCG- CAACTTAAAG

C5

1541 1610
H15 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
BZ10 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
BZ198 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
P20 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
H38 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
Z2491 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
H41 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
EG329 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
PMC21 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
EG327 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC
Consensus G-GTGGCGCA AAAC TTGAAC AACC-CATCG ACAATGTG-A CGGCAACGCG CG-GCGGG-A TCGCCCAAGC

C5

1611 1680
H15 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
BZ10 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
BZ198 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
P20 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
H38 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
Z2491 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
H41 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
EG329 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
PMC21 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
EG327 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA
Consensus GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA

C5

FIG. 2G

[illegible]

	1751						1815
H15	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
BZ10	GCACGGGCTC	CGGCAATTGG	CGCGGTCATT	TCGGTGACTTC	CGCATCTGTC	GGTATCAGT	GGTAA
BZ198	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
P20	GCACGGGCTC	CGGCAATTGG	CGCGGTCATT	TCGGTGACTTC	CGCATCTGTC	GGTATCAGT	GGTAA
H38	GCACGGGCTC	CGGCAATTGG	CGCGGTCATT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
Z2491	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
H41	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
EG329	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
PMC21	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
EG327	GCACGGGCTC	CGGCAATTGG	CGCGGCCAAT	TCGGTGCTTC	CGCATCTGTC	GGTATCAGT	GGTAA
Consensus	<u>GCACGGGCTC</u>	<u>CGGCAATTGG</u>	<u>CGCGGCCAAT</u>	<u>TCGGT-GCTTC</u>	<u>CGCATCTGTC</u>	<u>GGTATCA-T</u>	<u>GGTAA</u>

FIG. 2H



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1 50
H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN
PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVOAS
H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN
PMC21Bgldel MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS
PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS
C1

51 100
H41 ATDED...EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE
PMC21 ANNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
H41Studel ATDE.....
PMC21Bgldel ANNE.....
PMC21C1C5 AN.....
V1

101 150
H41 FVDPYIVVTI KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK
PMC21 GVLTAIREITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK
H41Studel TGLINVETEK
PMC21Bgldel TDLTSVGTEK
PMC21C1C5
V1 C2 V2 C3

151 200
H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
PMC21 LSFSAHGNKV NITS DT KGLN FAKETAGTNG DTTVHLNGIG STLTDLTLNT
H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
PMC21Bgldel LSFSAHGNKV NITS DT KGLN FAKETAGTNG DTTVHLNGIG STLTDLTLNT
PMC21C1C5
C3 V3

201 250
H41 GATTNVTDND VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21 GATTNVTDND VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
H41Studel GATTNVTDND VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21Bgldel GATTNVTDND VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21C1C5NVDFVRT
V3 C4 V4 C5

251 300
H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK
PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGD
H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK
PMC21Bgldel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGD
PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGD
C5

301 350
H41 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
PMC21 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
H41Studel KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
PMC21Bgldel KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
PMC21C1C5 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
C5

351 400
H41 SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD
PMC21 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD
H41Studel SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD
PMC21Bgldel SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD
PMC21C1C5 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD
C5

FIG. 10A



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401 450
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
C5

451 500
H41 TPOFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVVIT NVAPGVKEGD
PMC21 TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD
H41Studel TPOFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVVIT NVAPGVKEGD
PMC21Bgldel TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD
PMC21C1C5 TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD
C5

501 550
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21 VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA
C5

551 600
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYOW.
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYOW.
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYOW.
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYOW.
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYOW.
C5

FIG. 10B